

ID 053651 PRELIMINARY: PRT: 255 AA.
 AC 053651:
 DT 01-NOV-1996 (TREMblrel: 01, Created)
 DT 01-NOV-1996 (TREMblrel: 01, Last sequence update)
 DE CAMP FACTOR PRECURSOR.
 DE Streptococcus agalactiae.
 OS Bacteria: Firmicutes: Bacillus/Clostridium group: Streptococcaceae;
 OC Streptococcus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-R268:
 RA MEDLINE: 95231384.
 * POBBIESTI A.
 RT "Molecular characterization of the cfb gene encoding group B
 streptococcal CAMP-factor."
 RL Med. Microbiol. Immunol. 183:239-256(1994).
 DR EMBL: X72754; CAA51283.1;
 PT SIGNAL.
 .. MAIN 1 29 POTENTIAL.
 .. QUENCE 255 AA: 28373 MW: 5938126E CRC32:

Query Match 53.5%: Score 794.5; DB 2: Length 255;
 Best Local Similarity 63.0%: Pred. No. 1.2e+43;
 Matches 155: Conservative 37: Mismatches 47: Indels 13: Gaps 3:

Y 1 MEKRLLYTOS-AGITLSPILTSVQANQINVSOP-----PSNSESNIYSCKEEIDNS 54
 Db 1 MNVTHMYLGLTIGVAGLLEFSPAVLEHNDQVTPGVNHNVSNNQAOQMAK----- 54
 Y 55 LNOESAGLYALKEVDYKTEECESVNSAISEVENKTSLSAARETTIYDLSICIRVETASD 114
 Db 54 LDDSDIOLRNKKNVGGIDYKPVNENAIISVEKLTSLRANPEIYVDLSISREVALTD 113
 Y 115 VIGAVFSTQILNKVDCALHMGFAIKLRADPFASNSISGVEAVYQVQATVLT 174
 Db 114 VIEATFSTQHLNKVSQANIDMGFGITKLVIRIDPFASVSISKAQVNDVALEQKVL 173
 Y 175 YPDLPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 234
 Db 174 YPDLKPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 233
 Y 235 VTVAQVDEIKVQDEALNTAQ 256
 Db 234 VTVAQVDEIKVQDEALNTAQ 255
 RefSeq 3
 ID 086016 PRELIMINARY: PRT: 257 AA.
 AC 086016:
 DT 01-NOV-1998 (TREMblrel: 08, Created)
 DT 01-NOV-1998 (TREMblrel: 08, Last sequence update)
 DE CAMP FACTOR.
 DE Streptococcus agalactiae.
 OS Bacteria: Firmicutes: Bacillus/Clostridium group: Streptococcaceae;
 OC Streptococcus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SF370:
 RA GASE K., MCSHAN W.M., PRIMEAUX C., FERRETTI J.J.
 RT "The CAMP factor gene (cfa) of group A streptococci: Identification,
 cloning, and expression."
 RL Submitted (Jul-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF079502; AAC29481.1;
 SO SEQUENCE 257 AA: 28480 MW: EC5BD8E3 CRC32:

Best Local Similarity 55.6%: Pred. No. 2.7e+38;
 Matches 145: Conservative 51: Mismatches 55: Indels 13: Gaps 3:
 Y 1 MEKRLLYTOS-AGITLSPILTSVQANQINVSOP-----PSNSESNIYSCKEEIDNS 54
 Db 1 MKPKHLLSTSVAGLLEFSTMTSHVAD--DASNDALIMNNQAN 54
 Y 56 NQESAGLYALKEVDYKTEECESVNSAISEVENKTSLSAARETTIYDLSICIRVETASD 114
 Db 56 DEHQOLEAIKHEAKGIDITLVKKAIDAVDHKSSIRPNTETVD 113
 Y 116 IOAVFSTQILNKVDCALHMGFAIKLRADPFASNSISGVEAVYQVQATVLT 174
 Db 116 IKAVFSTQILNKVDCALHMGFAIKLRADPFASNSISGVEAVYQVQATVLT 173
 Y 176 PDLOPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 234
 Db 176 PDLOPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 233
 Y 236 VTVAQVDEIKVQDEALNTAQ 256
 Db 236 VTVAQVDEIKVQDEALNTAQ 255

RESULT 4
 ID P78969 PRELIMINARY: PRT: 1526 AA.
 AC P78969:
 DT 01-MAY-1997 (TREMblrel: 03, Created)
 DT 01-MAY-1997 (TREMblrel: 03, Last sequence update)
 DE MYOSIN II.
 GN MYO2.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Arctiascomycetes;
 OC Schizosaccharomycetes; Schizosaccharomycetaceae;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-972 H-1.
 RA MAY K.M., WATTS F.Z., JONES N., HYAMS J.S.
 RL Mol. Biol. Cell 0:0-0(1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-972 H-1.
 RX MEDLINE: 98075862.
 RA MAY K.M., WATTS F.Z., JONES N., HYAMS J.S.
 RT "Type II myosin involved in cytokinesis in the fission
 Schizosaccharomyces pombe."
 RL Cell Motil. Cytoskeleton 38:385-396(1997).
 DR EMBL: U75357; AAC49908.1;
 DR PFAM: PF00612; IO: 1.
 DR PFAM: PF00612; myosin-head: 1.
 SO SEQUENCE 1526 AA: 176499 MW: 10AF564F CRC32:

Query Match 5.3%: Score 116.5; DB 3: Length 257;
 Best Local Similarity 20.9%: Pred. No. 11;
 Matches 51: Conservative 61: Mismatches 83: Indels 13: Gaps 3:
 Y 52 DNSLNQESAGLYALKEVDYKTEECESVNSAISEVENKTSLSAARETTIYDLSICIRVETASD 114
 Db 823 DKOLKRDADIELKELKQONKSEVERDLVETNLSAVENLT 113
 Y 93 RANPETIYDLSIGTRVAVSIVQAVFSTQILNKVQAHIDMGF 174
 Db 883 PRIOERPLANEDSFSEKQONENKRESASLKOINNESELENTS 173
 Y 150 DPFAASNE-----SIKQVEAVKYQVQATVLT-----YPDLPTDRATITV 234
 Db 943 EKLSLEKDLDTKGELESIRENNATVLSKAEFNEQCKSLQETIVT 233
 Y 196 -----IMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPTV 233

Best Local Similarity	67.8%
Best Local Consistency	67.9%
Matches	361
Conservative	361
Probed No.	36-7
Mismatched	36-7
Matched	36-7

Db 998 TTCAATCCAAATGTAAGGTAAGAAAGTGAATGAATATTT
C7 907 TTAATACGTCCTGAAATGAATGAAGACT 337
Db 1058 CTTCAACGAGCATTAATATATATTTATTT 1058

RESULT 3
AF079502
LOCUS
DEFINITION
ACCESSION
NID
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
TITLE
JOURNAL

FEATURES
source

AF079402
Streptococcus faecalis
Streptococcus faecalis CAMP (type strain)
93406758
AF079502.1
Streptococcus faecalis
Streptococcus faecalis
Bacterial Firmicutes Bacillus/streptococcus
Streptococcus
1 (bases 1 to 1000)
Gase, K., Moshal, W.M., Fitzmaurice, J. and Petti
The CAMP test of *Staphylococcus aureus* and *Staphylococcus*
cloning, and expression
Unpublished
2 (bases 1 to 1000)
Gase, K., Moshal, W.M., Fitzmaurice, J. and Petti
Direct Submission
Submitted (22-JUL-1997) Microbiology and
Oklahoma Health Sciences Center 741 S.W.
City, OK 73109, USA
Location/Qualifiers
1 2100

[illegible]

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Query Match      25000 Sites 30000 Ch 10000
Best Local Similarity 50.00 Pct. No. 3634
Matches 555 Conserved 100 Mismatches 445

QY      32 TATTTTATGAAATATAATATTTGATTAAAAATTTTAA
      |||||
LB      557 TATTTTCGAAATTAATAAATATGCTTAAATAAAATAGT
QY      92 TAAGTACTATTATTTATATACATGCAATTTATATAAATA
      |||||
DB      717 TAAGGCTTAATAATTAATTAAGTTCCTTAAGCATTTAAATA
      |||||
QY      147 AGGATGCTTAATGCAATTAATAAATTAATTATTTAAATATTA
      |||||
DB      777 GAGGATTAATATGAACATAAATACCTCTCTGCTTCAATAGT
      |||||
QY      287 TTAATTTTCCCAATTTTAAATATTTCAAGCAATTAATAATAA
      |||||
DB      837 TTTATTTCAACATATAAGCATTAAGTTTAACTGATATATTTTA
      |||||

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